

UNITED STATES PATENT AND TRADEMARK OFFICE
CERTIFICATE OF CORRECTION

PATENT NO. : 6,994,857 B2
APPLICATION NO. : 09/833041
DATED : February 7, 2006
INVENTOR(S) : Craig A. Rosen and William A. Haseltine

Page 1 of 46

It is certified that error appears in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

Title page item (60), (Related U.S. Application Date) of the title page, delete the text beginning with "Provisional application No. 60/229,358" to and ending with "provisional application No. 60/256,931, filed on Dec. 1, 2000."

On page 7, column 2, in the 8th reference, delete the text beginning with "Hershfield, M.S., et al.," to and ending "7185-7189 (1991)" and insert -- Hochuli, E., "Interferon Immunogenicity: Technical Evaluation of Interferon- α 2a," *Journal of Interferon and Cytokine Research* 17:S15-S21 (1997). --

On page 10, column 2, after the 9th reference (Nilsson, J., et al.), insert -- Nilsson, J. et al., "Heat-Mediated Activation of Affinity-Immobilized Taq DNA Polymerase," *BioTechniques* 22:744-751 (1997). --

Title page item (57) (ABSTRACT) of the title page, "disordrs" should read -- disorders--.

In the Specification:

Col. 25 (Table 1), row HLD0U18, column Exemplary Identifier, "SEQ ID NO:73" should read -- SEQ ID NO:74 --.

Col.27 (Table 1), row HWACB86, column Exemplary Identifier, "SEQ ID NO 74" should read -- SEQ ID NO:75 --.

Col. 27 (Table 1), row HCEGG08, column Exemplary Identifier, "SEQ ID NO:75" should read -- SEQ ID NO:76 --.

Col. 29 (Table 1), row HWHGZ51, column Exemplary Identifier, "SEQ ID NO:76" should read -- SEQ ID NO:77 --.

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PATENT NO. : 6,994,857 B2
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DATED : February 7, 2006
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Page 2 of 46

It is certified that error appears in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

Col. 29 (Table 1), row HDTAI21, column Exemplary Identifier, "SEQ ID NO: 77" should read -- SEQ ID NO: 78 --.

Col. 29 (Table 1), row HCNCA73, column Exemplary Identifier, "SEQ ID NO: 78" should read -- SEQ ID NO: 79 --.

Col. 29 (Table 1), row HNHFE71, column Exemplary Identifier, "SEQ ID NO: 79" should read -- SEQ ID NO: 80--.

Col. 62, lines 38-39, "(SEQ ID NO:36)" should read -- (SEQ ID NO:72) --.

Col. 215, line 8, "(SEQ ID NO:36)" should read -- (SEQ ID NO:81) --.

Col. 236, line 42, "(SEQ ID NO:37)" should read -- (SEQ ID NO:82) --.

Col. 237, line 47, "(SEQ ID NO:38)" should read -- (SEQ ID NO:83) --.

Col. 237, lines 53-54, "(SEQ ID NO:39)" should read -- (SEQ ID NO:84) --.

Col. 237, line 63, "(SEQ ID NO:40)" should read -- (SEQ ID NO:85) --.

Col. 240, line 55, "(SEQ ID NO:41)" should read -- (SEQ ID NO:86) --.

Col. 240, line 58, "(SEQ ID NO:42)" should read -- (SEQ ID NO:87) --.

Col. 243, line 9, "(SEQ ID NO:43)" should read -- (SEQ ID NO:88) --.

Col. 243, line 14, "(SEQ ID NO:44)" should read -- (SEQ ID NO:89) --.

Col. 243, lines 17-18, "(SEQ ID NO:39)" should read -- (SEQ ID NO:84) --.

Col. 243, line 28, "(SEQ ID NO:45)" should read -- (SEQ ID NO:90) --.

In the Sequence Listing:

Delete the Sequence Listing beginning in Col. 263, with the text "<160> NUMBER OF SEQ ID NOS:79" to and ending "

Pro Thr Ser Cys Ser Arg Cys "
165

In Col. 313 and insert the following Sequence Listing:

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<160> NUMBER OF SEQ ID NOS: 90

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<211> 23

<212> DNA

<213> Artificial Sequence

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<221> primer_bind
<223> primer useful to clone human growth hormone cDNA

<400> 1
cccaagaatt cccttatcca ggc

23

<210> 2
<211> 33
<212> DNA
<213> Artificial Sequence
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<221> primer_bind
<223> primer useful to clone human growth hormone cDNA

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33

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<211> 16
<212> DNA
<213> Artificial Sequence
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<221> misc_structure
<223> synthetic oligonucleotide used to join DNA fragments
with non-cohesive ends.

<400> 3
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16

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<211> 17
<212> DNA
<213> Artificial Sequence
<220>
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<223> synthetic oligonucleotide used to join DNA fragments
with non-cohesive ends.

<400> 4
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17

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<213> Artificial Sequence
<220>
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<223> synthetic oligonucleotide used to join DNA fragments with non-cohesive ends.

<400> 5

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17

<210> 6

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<221> misc_structure

<223> synthetic oligonucleotide used to join DNA fragments with non-cohesive ends.

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<211> 24

<212> PRT

<213> Artificial Sequence

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<221> SITE

<222> 1)..(19)

<223> invertase leader sequence

<220>

<221> SITE

<222> 20)..(24)

<223> first 5 amino acids of mature human serum albumin

<400> 7

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5

10

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Ile Ser Ala Asp Ala His Lys Ser

20

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<211> 21

<212> DNA

<213> Artificial Sequence

<220>

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<223> synthetic oligonucleotide used to join DNA fragments with non-cohesive ends.

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<221> misc_structure
<223> synthetic oligonucleotide used to join DNA
fragments with non-cohesive ends.

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27

<210> 10
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fragments with non-cohesive ends.

<400> 10
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24

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<223> synthetic oligonucleotide used to join DNA
fragments with non-cohesive ends.

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30

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<211> 31
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<213> Artificial Sequence
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fragments with non-cohesive ends.

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31

<210> 13
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 <213> Artificial Sequence
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 <221> misc_structure
 <223> synthetic oligonucleotide used to join DNA
 fragments with non-cohesive ends.

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47

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 <211> 48
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 <213> Artificial Sequence
 <220>
 <221> misc_structure
 <223> synthetic oligonucleotide used to join DNA
 fragments with non-cohesive ends.

<400> 14
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48

<210> 15
 <211> 62
 <212> DNA
 <213> Artificial Sequence
 <220>
 <221> misc_structure
 <223> synthetic oligonucleotide used to join DNA
 fragments with non-cohesive ends.

<400> 15
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 ac 62

<210> 16
 <211> 63
 <212> DNA
 <213> Artificial Sequence
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 <221> misc_structure
 <223> synthetic oligonucleotide used to join DNA
 fragments with non-cohesive ends.

<400> 16
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gcc

63

<210> 17

<211> 1782

<212> DNA

<213> Homo sapiens

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<222> (1)..(1755)

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1 5 10 15	
 gaa aat ttc aaa gcc ttg gtg ttg att gcc ttt gct cag tat ctt cag	96
Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln	
20 25 30	
 cag tgt cca ttt gaa gat cat gta aaa tta gtg aat gaa gta act gaa	144
Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu	
35 40 45	
 ttt gca aaa aca tgt gtt gct gat gag tca gct gaa aat tgt gac aaa	192
Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys	
50 55 60	
 tca ctt cat acc ctt ttt gga gac aaa tta tgc aca gtt gca act ctt	240
Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu	
65 70 75 80	
 cgt gaa acc tat ggt gaa atg gct gac tgc tgt gca aaa caa gaa cct	288
Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro	
85 90 95	
 gag aga aat gaa tgc ttc ttg caa cac aaa gat gac aac cca aac ctc	336
Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu	
100 105 110	
 ccc cga ttg gtg aga cca gag gtt gat gtg atg tgc act gct ttt cat	384
Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His	
115 120 125	
 gac aat gaa gag aca ttt ttg aaa aaa tac tta tat gaa att gcc aga	432
Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg	
130 135 140	
 aga cat cct tac ttt tat gcc ccg gaa ctc ctt ttc ttt gct aaa agg	480
Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg	
145 150 155 160	

tat aaa gct gct ttt aca gaa tgt tgc caa gct gct gat aaa gct gcc	528
Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala	
165 170 175	
tgc ctg ttg cca aag ctc gat gaa ctt cgg gat gaa ggg aag gct tcg	576
Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser	
180 185 190	
tct gcc aaa cag aga ctc aaa tgt gcc agt ctc caa aaa ttt gga gaa	624
Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu	
195 200 205	
aga gct ttc aaa gca tgg gca gtg gct cgc ctg agc cag aga ttt ccc	672
Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro	
210 215 220	
aaa gct gag ttt gca gaa gtt tcc aag tta gtg aca gat ctt acc aaa	720
Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys	
225 230 235 240	
gtc cac acg gaa tgc tgc cat gga gat ctg ctt gaa tgt gct gat gac	768
Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp	
245 250 255	
agg gcg gac ctt gcc aag tat atc tgt gaa aat cag gat tcg atc tcc	816
Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser	
260 265 270	
agt aaa ctg aag gaa tgc tgt gaa aaa cct ctg ttg gaa aaa tcc cac	864
Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His	
275 280 285	
tgc att gcc gaa gtg gaa aat gat gag atg cct gct gac ttg cct tca	912
Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser	
290 295 300	
tta gct gct gat ttt gtt gaa agt aag gat gtt tgc aaa aac tat gct	960
Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala	
305 310 315 320	
gag gca aag gat gtc ttc ctg ggc atg ttt ttg tat gaa tat gca aga	1008
Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg	
325 330 335	
agg cat cct gat tac tct gtc gtg ctg ctg ctg aga ctt gcc aag aca	1056
Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr	
340 345 350	
tat gaa acc act cta gag aag tgc tgt gcc gct gca gat cct cat gaa	1104
Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu	
355 360 365	

tgc tat gcc aaa gtg ttc gat gaa ttt aaa cct ctt gtg gaa gag cct	1152
Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro	
370 375 380	
cag aat tta atc aaa caa aac tgt gag ctt ttt gag cag ctt gga gag	1200
Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu	
385 390 395 400	
tac aaa ttc cag aat gcg cta tta gtt cgt tac acc aag aaa gta ccc	1248
Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro	
405 410 415	
caa gtg tca act cca act ctt gta gag gtc tca aga aac cta gga aaa	1296
Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys	
420 425 430	
gtg ggc agc aaa tgt tgt aaa cat cct gaa gca aaa aga atg ccc tgt	1344
Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys	
435 440 445	
gca gaa gac tat cta tcc gtg gtc ctg aac cag tta tgt gtg ttg cat	1392
Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His	
450 455 460	
gag aaa acg cca gta agt gac aga gtc aca aaa tgc tgc aca gag tcc	1440
Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser	
465 470 475 480	
ttg gtg aac agg cga cca tgc ttt tca gct ctg gaa gtc gat gaa aca	1488
Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr	
485 490 495	
tac gtt ccc aaa gag ttt aat gct gaa aca ttc acc ttc cat gca gat	1536
Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp	
500 505 510	
ata tgc aca ctt tct gag aag gag aga caa atc aag aaa caa act gca	1584
Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala	
515 520 525	
ctt gtt gag ctt gtg aaa cac aag ccc aag gca aca aaa gag caa ctg	1632
Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu	
530 535 540	
aaa gct gtt atg gat gat ttc gca gct ttt gta gag aag tgc tgc aag	1680
Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys	
545 550 555 560	
gct gac gat aag gag acc tgc ttt gcc gag gag ggt aaa aaa ctt gtt	1728
Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val	
565 570 575	

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 580 585

<210> 18
 <211> 585
 <212> PRT
 <213> Homo Sapiens

<400> 18

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Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
 20 25 30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
 35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
 50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
 65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
 85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
 100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
 115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
 130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
 145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
 165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
 180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
 195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
 210 215 220

Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
 225 230 235 240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
 245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
 260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
 275 280 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
 290 295 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
 305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
 325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
 340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
 355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
 370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
 385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
 405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
 420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
 435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
 450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
 465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
 485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
 500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
 515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
 530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
 545 550 555 560

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 565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu
 580 585

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<211> 58

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<213> Artificial Sequence

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<223> primer used to generate XhoI and ClaI
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<210> 21

<211> 24

<212> DNA

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<223> primer used in generation XhoI and ClaI

site in pPPC0006

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24

<210> 22

<211> 29

<212> DNA

<213> Artificial Sequence

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<221> primer_bind

<223> primer used in generation XhoI and ClaI
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<210> 23

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<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide used to alter restriction
sites in pPPC0007

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<210> 25

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<223> forward primer useful for generation of albumin

fusion protein in which the albumin moiety is N-terminal
of the Therapeutic Protein

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<212> DNA

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<223> reverse primer useful for generation of albumin fusion protein in which the albumin moiety is N-terminal of the Therapeutic Protein

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<210> 27
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<223> forward primer useful for generation of albumin fusion
protein in which the albumin moiety is c-terminal of the
Therapeutic Protein

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<400> 27
aggagcgtcg acaaaagann nnnnnnnnnn nnn

33

<210> 28
<211> 52
<212> DNA

<213> Artificial Sequence

<220>

<221> primer_bind

<223> reverse primer useful for generation of albumin fusion protein in which the albumin moiety is c-terminal of the Therapeutic Protein

<220>

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<222> (38)

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 ctttaaatacg atgagcaacc tcactcttgt gtgcatacnnn nnnnnnnnnn nn 52

<210> 29
 <211> 24
 <212> PRT
 <213> Artificial Sequence
 <220>
 <221> signal
 <223> signal peptide of natural human serum albumin protein

<400> 29
 Met Lys Trp Val Ser Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
 1 5 10 15

Tyr Ser Arg Ser Leu Asp Lys Arg
 20

<210> 30
 <211> 114
 <212> DNA

<213> Artificial Sequence

<220>

<221> primer_bind

<223> forward primer useful for generation of PC4:HSA
albumin fusion VECTOR

<220>

<221> misc_feature

<222> (5)..(10)

<223> BamHI restriction site

<220>

<221> misc_feature

<222> (11)..(16)

<223> Hind III restriction site

<220>

<221> misc_feature

<222> (17)..(27)

<223> Kozak sequence

<220>

<221> misc_feature

<222> (25)..(97)

<223> cds natural signal sequence of human serum albumin

<220>

<221> misc_feature

<222> (75)..(81)

<223> XhoI restriction site

<220>

<221> misc_feature

<222> (98)..(114)

<223> cds first six amino acids of human serum albumin

<400> 30

tcagggatcc aagcttccgc caccatgaag tgggtaacct ttatttcctt tctttttctc 60

tttagctcgg cttactcgag ggggtgtgtt cgtcgagatg cacacaagag tgag 114

<210> 31

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<221> primer_bind

<223> reverse primer useful for generation of
PC4:HSA albumin fusion VECTOR

<220>
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<222> (6)..(11)
<223> Asp718 restriction site

<220>
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<222> (12)..(17)
<223> BcoRI restriction site

<220>
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<222> (15)..(17)
<223> reverse complement of stop codon

<220>
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<222> (18)..(25)
<223> AscI restriction site

<220>
<221> misc_feature
<222> (18)..(43)
<223> reverse complement of DNA sequence encoding last 9 amino acids

<400> 31
gcagcggtac cgaattcggc gcgccttata agcctaaggc agc

43

<210> 32
<211> 46
<212> DNA
<213> Artificial Sequence
<220>

<221> primer_bind
<223> forward primer useful for inserting Therapeutic
protein into pC4:HSA vector

<220>
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<223> n equals a,t,g, or c

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<222> (46)
<223> n equals a,t,g, or c

<400> 32
ccgccgctcg aggggtgtgt ttcgtcgann nnnnnnnnnn nnnnnn

46

<210> 33
<211> 55
<212> DNA
<213> Artificial Sequence
<220>
<221> primer_bind
<223> reverse primer useful for inserting Therapeutic
protein into pC4:HSA vector

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<222> (38)
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<223> n equals a,t,g, or c

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<210> 34

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<221> signal

<223> Stanniocalcin signal peptide

<400> 34

Met Leu Gln Asn Ser Ala Val Leu Leu Leu Leu Val Ile Ser Ala Ser
1 5 10 15

Ala

<210> 35

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<221> signal

<223> Synthetic signal peptide

<400> 35

Met Pro Thr Trp Ala Trp Trp Leu Phe Leu Val Leu Leu Leu Ala Leu
1 5 10 15

Trp Ala Pro Ala Arg Gly
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<210> 36
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<221>primer_bind
<223>Degenerate VH forward primer useful for
amplifying human VH domains

<400> 36
caggtgcagc tggcgcagtc tgg 23

<210> 37
<211> 23
<212> DNA
<213> Artificial Sequence
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<221>primer_bind
<223>Degenerate VH forward primer useful for
amplifying human VH domains

<400> 37
caggtcaact taaggagtc tgg 23

<210> 38
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<221>primer_bind
<223>Degenerate VH forward primer useful for
amplifying human VH domains

<400> 38
gaggtgcagc tggcgcagtc tgg 23

<210> 39
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<221>primer_bind
<223>Degenerate VH forward primer useful for
amplifying human VH domains

<400> 39

caggtgcagc tgcaggagtc ggg

23

<210> 40

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<221>primer_bind

<223>Degenerate VH forward primer useful for
amplifying human VH domains

<400> 40

gaggtgcagc tgttgcagtc tgc

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<210> 41

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<221>primer_bind

<223>Degenerate VH forward primer useful for
amplifying human VH domains

<400> 41

caggtacagc tgcagcagtc agg

23

<210> 42

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<221>primer_bind

<223>Degenerate JH reverse primer useful for
amplifying human VH domains

<400> 42

tgaggagacg gtgaccaggg tgcc

24

<210> 43

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<221>primer_bind

<223>Degenerate JH reverse primer useful for
amplifying human VH domains

<400> 43

tgaagagacg gtgaccattg tccc

24

<210> 44

<211> 24
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<400> 44
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<210> 45
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<400> 45
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<210> 46
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
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 <223>Degenerate Vkappa forward primer useful for
 amplifying human VL domains

<400> 46
 gacatccaga tgacccagtc tcc 23

<210> 47
 <211> 23
 <212> DNA
 <213> Artificial Sequence
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<400> 47
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<210> 48
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<221>primer_bind
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amplifying human VL domains

<400> 48
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<210> 49
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amplifying human VL domains

<400> 49
gaaattgtgt tgacgcagtc tcc 23

<210> 50
<211> 23
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amplifying human VL domains

<400> 50
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<210> 51
<211> 23
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<223>Degenerate Vkappa forward primer useful for
amplifying human VL domains

<400> 51
gaaacgacac tcacgcagtc tcc 23

<210> 52
<211> 23
<212> DNA
<213> Artificial Sequence
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<221>primer_bind
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amplifying human VL domains

<400> 52
gaaattgtgc tgactcagtc tcc 23

<210> 53
<211> 23
<212> DNA
<213> Artificial Sequence
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amplifying human VL domains

<400> 53
cagtctgtgt tgacgcagcc gcc 23

<210> 54
<211> 23
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<213> Artificial Sequence
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amplifying human VL domains

<400> 54
cagtctgccc tgactcagcc tgc 23

<210> 55
<211> 23
<212> DNA
<213> Artificial Sequence
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<221>primer_bind
<223>Degenerate Vlambda forward primer useful for
amplifying human VL domains

<400> 55
tcctatgtgc tgactcagcc acc 23

<210> 56
<211> 23
<212> DNA
<213> Artificial Sequence
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<223>Degenerate Vlambda forward primer useful for
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<400> 56
tcttctgagc tgactcagga ccc 23

<210> 57

<211> 23
<212> DNA
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<400> 57
cacgttatac tgactcaacc gcc 23

<210> 58
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<400> 58
caggctgtgc tcactcagcc gtc 23

<210> 59
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<400> 59
aattttatgc tgactcagcc cca 23

<210> 60
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<400> 60
acgtttgatt tccaccttgg tccc 24

<210> 61
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<400> 61
acgtttgatc tccagcttgg tccc 24

<210> 62
<211> 24
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amplifying human VL domains

<400> 62
acgtttgata tccactttgg tccc 24

<210> 63
<211> 24
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amplifying human VL domains

<400> 63
acgtttgatc tccaccttgg tccc 24

<210> 64
<211> 24
<212> DNA
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amplifying human VL domains

<400> 64
acgtttaatc tccagtcgtg tccc 24

<210> 65
<211> 23
<212> DNA
<213> Artificial Sequence
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<223>Degenerate Jlambda reverse primer useful for
amplifying human VL domains

<400> 65
cagtctgtgt tgacgcagcc gcc 23

<210> 66
<211> 23
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amplifying human VL domains

<400> 66
cagtctgccc tgactcagcc tgc 23

<210> 67
<211> 23
<212> DNA
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amplifying human VL domains

<400> 67
tcctatgtgc tgactcagcc acc 23

<210> 68
<211> 23
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amplifying human VL domains

<400> 68
tcttctgagc tgactcagga ccc 23

<210> 69
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amplifying human VL domains

<400> 69
cacgttatac tgactcaacc gcc 23

<210> 70

<211> 23
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<400> 70
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<210> 71
 <211> 23
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 <221>primer_bind
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<400> 71
 aattttatgc tgactcagcc cca 23

<210> 72
 <211> 15
 <212> PRT
 <213> Artificial Sequence
 <220>
 <221>turn
 <223>Linker peptide that may be used to join VH
 and VL domains in an scFv.

<400> 72
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1 5 10 15

<210> 73
 <211> 23
 <212> PRT
 <213> Homo sapiens

<400> 73
 Cys Cys Cys Ala Ala Gly Ala Ala Thr Thr Cys Cys Cys Thr Thr Ala
 1 5 10 15

Thr Cys Cys Ala Gly Gly Cys
 20

<210> 74
 <211> 429
 <212> PRT

<213> Homo sapiens

<400> 74

Met	Cys	Pro	Gly	Ala	Leu	Trp	Val	Ala	Leu	Pro	Leu	Leu	Ser	Leu	Leu	1	5	10	15
Ala	Gly	Ser	Leu	Gln	Gly	Lys	Pro	Leu	Gln	Ser	Trp	Gly	Arg	Gly	Ser	20	25	30	
Ala	Gly	Gly	Asn	Ala	His	Ser	Pro	Leu	Gly	Val	Pro	Gly	Gly	Gly	Leu	35	40	45	
Pro	Glu	His	Thr	Phe	Asn	Leu	Lys	Met	Phe	Leu	Glu	Asn	Val	Lys	Val	50	55	60	
Asp	Phe	Leu	Arg	Ser	Leu	Asn	Leu	Ser	Gly	Val	Pro	Ser	Gln	Asp	Lys	65	70	75	80
Thr	Arg	Val	Glu	Pro	Pro	Gln	Tyr	Met	Ile	Asp	Leu	Tyr	Asn	Arg	Tyr	85	90	95	
Thr	Ser	Asp	Lys	Ser	Thr	Thr	Pro	Ala	Ser	Asn	Ile	Val	Arg	Ser	Phe	100	105	110	
Ser	Met	Glu	Asp	Ala	Ile	Ser	Ile	Thr	Ala	Thr	Glu	Asp	Phe	Pro	Phe	115	120	125	
Gln	Lys	His	Ile	Leu	Leu	Phe	Asn	Ile	Ser	Ile	Pro	Arg	His	Glu	Gln	130	135	140	
Ile	Thr	Arg	Ala	Glu	Leu	Arg	Leu	Tyr	Val	Ser	Cys	Gln	Asn	His	Val	145	150	155	160
Asp	Pro	Ser	His	Asp	Leu	Lys	Gly	Ser	Val	Val	Ile	Tyr	Asp	Val	Leu	165	170	175	
Asp	Gly	Thr	Asp	Ala	Trp	Asp	Ser	Ala	Thr	Glu	Thr	Lys	Thr	Phe	Leu	180	185	190	
Val	Ser	Gln	Asp	Ile	Gln	Asp	Glu	Gly	Trp	Glu	Thr	Leu	Glu	Val	Ser	195	200	205	
Ser	Ala	Val	Lys	Arg	Trp	Val	Arg	Ser	Asp	Ser	Thr	Lys	Ser	Lys	Asn	210	215	220	
Lys	Leu	Glu	Val	Thr	Val	Glu	Ser	His	Arg	Lys	Gly	Cys	Asp	Thr	Leu	225	230	235	240
Asp	Ile	Ser	Val	Pro	Pro	Gly	Ser	Arg	Asn	Leu	Pro	Phe	Phe	Val	Val	245	250	255	

Phe Ser Asn Asp His Ser Ser Gly Thr Lys Glu Thr Arg Leu Glu Leu
 260 265 270

Arg Glu Met Ile Ser His Glu Gln Glu Ser Val Leu Lys Lys Leu Ser
 275 280 285

Lys Asp Gly Ser Thr Glu Ala Gly Glu Ser Ser His Glu Glu Asp Thr
 290 295 300

Asp Gly His Val Ala Ala Gly Ser Thr Leu Ala Arg Arg Lys Arg Ser
 305 310 315 320

Ala Gly Ala Gly Ser His Cys Gln Lys Thr Ser Leu Arg Val Asn Phe
 325 330 335

Glu Asp Ile Gly Trp Asp Ser Trp Ile Ile Ala Pro Lys Glu Tyr Glu
 340 345 350

Ala Tyr Glu Cys Lys Gly Gly Cys Phe Phe Pro Leu Ala Asp Asp Val
 355 360 365

Thr Pro Thr Lys His Ala Ile Val Gln Thr Leu Val His Leu Lys Phe
 370 375 380

Pro Thr Lys Val Gly Lys Ala Cys Cys Val Pro Thr Lys Leu Ser Pro
 385 390 395 400

Ile Ser Val Leu Tyr Lys Asp Asp Met Gly Val Pro Thr Leu Lys Tyr
 405 410 415

His Tyr Glu Gly Met Ser Val Ala Glu Cys Gly Cys Arg
 420 425

<210> 75

<211> 280

<212> PRT

<213> Homo sapiens

<400> 75

Met Ala Pro Ser Gly Ser Leu Ala Val Pro Leu Ala Val Leu Val Leu
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Leu Leu Trp Gly Ala Pro Trp Thr His Gly Arg Arg Ser Asn Val Arg
 20 25 30

Val Ile Thr Asp Glu Asn Trp Arg Glu Leu Leu Glu Gly Asp Trp Met
 35 40 45

Ile Glu Phe Tyr Ala Pro Trp Cys Pro Ala Cys Gln Asn Leu Gln Pro
 50 55 60

Glu Trp Glu Ser Phe Ala Glu Trp Gly Glu Asp Leu Glu Val Asn Ile
 65 70 75 80

Ala Lys Val Asp Val Thr Glu Gln Pro Gly Leu Ser Gly Arg Phe Ile
 85 90 95

Ile Thr Ala Leu Pro Thr Ile Tyr His Cys Lys Asp Gly Glu Phe Arg
 100 105 110

Arg Tyr Gln Gly Pro Arg Thr Lys Lys Asp Phe Ile Asn Phe Ile Ser
 115 120 125

Asp Lys Glu Trp Lys Ser Ile Glu Pro Val Ser Ser Trp Phe Gly Pro
 130 135 140

Gly Ser Val Leu Met Ser Ser Met Ser Ala Leu Phe Gln Leu Ser Met
 145 150 155 160

Trp Ile Arg Thr Cys His Asn Tyr Phe Ile Glu Asp Leu Gly Leu Pro
 165 170 175

Val Trp Gly Ser Tyr Thr Val Phe Ala Leu Ala Thr Leu Phe Ser Gly
 180 185 190

Leu Leu Leu Gly Leu Cys Met Ile Phe Val Ala Asp Cys Leu Cys Pro
 195 200 205

Ser Lys Arg Arg Arg Pro Gln Pro Tyr Pro Tyr Pro Ser Lys Lys Leu
 210 215 220

Leu Ser Glu Ser Ala Gln Pro Leu Lys Lys Val Glu Glu Glu Gln Glu
 225 230 235 240

Ala Asp Glu Glu Asp Val Ser Glu Glu Glu Ala Glu Ser Lys Glu Gly
 245 250 255

Thr Asn Lys Asp Phe Pro Gln Asn Ala Ile Arg Gln Arg Ser Leu Gly
 260 265 270

Pro Ser Leu Ala Thr Asp Lys Ser
 275 280

<210> 76

<211> 112

<212> PRT

<213> Homo sapiens

<400> 76

Met Phe Trp Val Met Glu Thr Ala Lys Pro Pro Val Ser Glu Asp Ser
 1 5 10 15

Phe Arg Leu Pro Arg Lys Trp Gly Trp Arg Thr Glu Ala Thr Ala Pro
 20 25 30

His Ala Pro Val Pro Gln Ser Ile Cys Pro Arg Tyr Thr Ser Pro Cys
 35 40 45

Ala Pro His Asp Cys Gly Ser Gln Thr Val Gln Gly Asn Ser Leu Ser
 50 55 60

Leu Phe Tyr Thr Leu Ser His Lys Ala Pro Gln Leu Pro His Arg Val
 65 70 75 80

Pro Ala Pro Leu Phe Cys Lys Tyr Val Lys Arg Lys Lys Cys Lys Arg
 85 90 95

Trp Ser Leu Gly Trp Ser Ser Ser Leu Gln Leu Arg Leu Leu Thr Met
 100 105 110

<210> 77

<211> 346

<212> PRT

<213> Homo sapiens

<400> 77

Met Asp Pro Ala Arg Lys Ala Gly Ala Gln Ala Met Ile Trp Thr Ala
 1 5 10 15

Gly Trp Leu Leu Leu Leu Leu Leu Arg Gly Gly Ala Gln Ala Leu Glu
 20 25 30

Cys Tyr Ser Cys Val Gln Lys Ala Asp Asp Gly Cys Ser Pro Asn Lys
 35 40 45

Met Lys Thr Val Lys Cys Ala Pro Gly Val Asp Val Cys Thr Glu Ala
 50 55 60

Val Gly Ala Val Glu Thr Ile His Gly Gln Phe Ser Leu Ala Val Arg
 65 70 75 80

Gly Cys Gly Ser Gly Leu Pro Gly Lys Asn Asp Arg Gly Leu Asp Leu
 85 90 95

His Gly Leu Leu Ala Phe Ile Gln Leu Gln Gln Cys Ala Gln Asp Arg
 100 105 110

Cys Asn Ala Lys Leu Asn Leu Thr Ser Arg Ala Leu Asp Pro Ala Gly
 115 120 125

Asn Glu Ser Ala Tyr Pro Pro Asn Gly Val Glu Cys Tyr Ser Cys Val
 130 135 140

Gly Leu Ser Arg Glu Ala Cys Gln Gly Thr Ser Pro Pro Val Val Ser
 145 150 155 160

Cys Tyr Asn Ala Ser Asp His Val Tyr Lys Gly Cys Phe Asp Gly Asn
 165 170 175

Val Thr Leu Thr Ala Ala Asn Val Thr Val Ser Leu Pro Val Arg Gly
 180 185 190

Cys Val Gln Asp Glu Phe Cys Thr Arg Asp Gly Val Thr Gly Pro Gly
 195 200 205

Phe Thr Leu Ser Gly Ser Cys Cys Gln Gly Ser Arg Cys Asn Ser Asp
 210 215 220

Leu Arg Asn Lys Thr Tyr Phe Ser Pro Arg Ile Pro Pro Leu Val Arg
 225 230 235 240

Leu Pro Pro Pro Glu Pro Thr Thr Val Ala Ser Thr Thr Ser Val Thr
 245 250 255

Thr Ser Thr Ser Ala Pro Val Arg Pro Thr Ser Thr Thr Lys Pro Met
 260 265 270

Pro Ala Pro Thr Ser Gln Thr Pro Arg Gln Gly Val Glu His Glu Ala
 275 280 285

Ser Arg Asp Glu Glu Pro Arg Leu Thr Gly Gly Ala Ala Gly His Gln
 290 295 300

Asp Arg Ser Asn Ser Gly Gln Tyr Pro Ala Lys Gly Gly Pro Gln Gln
 305 310 315 320

Pro His Asn Lys Gly Cys Val Ala Pro Thr Ala Gly Leu Ala Ala Leu
 325 330 335

Leu Leu Ala Val Ala Ala Gly Val Leu Leu
 340 345

<210> 78

<211> 272

<212> PRT

<213> Homo sapiens

<400> 78

Met Lys Gly Lys Lys Gly Ile Val Ala Ala Ser Gly Ser Glu Thr Glu
 1 5 10 15

Asp Glu Asp Ser Met Asp Ile Pro Leu Asp Leu Ser Ser Ser Ala Gly
 20 25 30

Ser Gly Lys Arg Arg Arg Arg Gly Asn Leu Pro Lys Glu Ser Val Gln
 35 40 45
 Ile Leu Arg Asp Trp Leu Tyr Glu His Arg Tyr Asn Ala Tyr Pro Ser
 50 55 60
 Glu Gln Glu Lys Ala Leu Leu Ser Gln Gln Thr His Leu Ser Thr Leu
 65 70 75 80
 Gln Val Cys Asn Trp Phe Ile Asn Ala Arg Arg Arg Leu Leu Pro Asp
 85 90 95
 Met Leu Arg Lys Asp Gly Lys Asp Pro Asn Gln Phe Thr Ile Ser Arg
 100 105 110
 Arg Gly Ala Lys Ile Ser Glu Thr Ser Ser Val Glu Ser Val Met Gly
 115 120 125
 Ile Lys Asn Phe Met Pro Ala Leu Glu Glu Thr Pro Phe His Ser Cys
 130 135 140
 Thr Ala Gly Pro Asn Pro Thr Leu Gly Arg Pro Leu Ser Pro Lys Pro
 145 150 155 160
 Ser Ser Pro Gly Ser Val Leu Ala Arg Pro Ser Val Ile Cys His Thr
 165 170 175
 Thr Val Thr Ala Leu Lys Asp Val Pro Phe Ser Leu Cys Gln Ser Val
 180 185 190
 Gly Val Gly Gln Asn Thr Asp Ile Gln Gln Ile Ala Ala Lys Asn Phe
 195 200 205
 Thr Asp Thr Ser Leu Met Tyr Pro Glu Asp Thr Cys Lys Ser Gly Pro
 210 215 220
 Ser Thr Asn Thr Gln Ser Gly Leu Phe Asn Thr Pro Pro Pro Thr Pro
 225 230 235 240
 Pro Asp Leu Asn Gln Asp Phe Ser Gly Phe Gln Leu Leu Val Asp Val
 245 250 255
 Ala Leu Lys Arg Ala Ala Glu Met Glu Leu Gln Ala Lys Leu Thr Ala
 260 265 270

<210> 79

<211> 167

<212> PRT

<213> Homo sapiens

<400> 79

Met Leu Thr Val Ala Leu Leu Ala Leu Leu Cys Ala Ser Ala Ser Gly
 1 5 10 15

Asn Ala Ile Gln Ala Arg Ser Ser Ser Tyr Ser Gly Glu Tyr Gly Gly
 20 25 30

Gly Gly Gly Lys Arg Phe Ser His Ser Gly Asn Gln Leu Asp Gly Pro
 35 40 45

Ile Thr Ala Leu Arg Val Arg Val Asn Thr Tyr Tyr Ile Val Gly Leu
 50 55 60

Gln Val Arg Tyr Gly Lys Val Trp Ser Asp Tyr Val Gly Gly Arg Asn
 65 70 75 80

Gly Asp Leu Glu Glu Ile Phe Leu His Pro Gly Glu Ser Val Ile Gln
 85 90 95

Val Ser Gly Lys Tyr Lys Trp Tyr Leu Lys Lys Leu Val Phe Val Thr
 100 105 110

Asp Lys Gly Arg Tyr Leu Ser Phe Gly Lys Asp Ser Gly Thr Ser Phe
 115 120 125

Asn Ala Val Pro Leu His Pro Asn Thr Val Leu Arg Phe Ile Ser Gly
 130 135 140

Arg Ser Gly Ser Leu Ile Asp Ala Ile Gly Leu His Trp Asp Val Tyr
 145 150 155 160

Pro Thr Ser Cys Ser Arg Cys
 165

<210> 80

<211> 22

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (22)

<223> Xaa equals stop translation

<400> 80

Met Leu Ala Ala Leu Ala Cys Ser Trp Arg Leu Leu Ser Leu Gly Ala
 1 5 10 15

His Ser Gly Arg Ala Xaa
 20

<210> 81

<211> 733
 <212> DNA
 <213> Homo sapiens

<400> 81
 gggatccgga gcccaaattct tctgacaaaa ctcacacatg cccaccgtgc ccagcacctg 60
 aattcgaggg tgcaccgtca gtcttctctt tcccccaaa acccaaggac accctcatga 120
 tctcccgga tcttgaggtc acatgcgtgg tgggtggacgt aagccacgaa gaccctgagg 180
 tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca aagccgcggg 240
 aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg caccaggact 300
 ggctgaatgg caaggagtac aagtgcaagg tctccaacaa agccctccca acccccatcg 360
 agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc 420
 catcccgga tgagctgacc aagaaccagg tcagcctgac ctgcctggtc aaaggcttct 480
 atccaagcga catcgccgtg gagtgggaga gcaatgggca gccgggagac aactacaaga 540
 ccacgcctcc cgtgctggac tccgacggct ccttcttctt ctacagcaag ctcaccgtgg 600
 acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat gaggctctgc 660
 acaaccacta cagcgagaag agcctctccc tgtctccggg taaatgagtg cgacggccgc 720
 gactctagag gat

<210> 82
 <211> 5
 <212> PRT
 <213> Artificial sequence
 <220>
 <221> misc_structure
 <223> membrane proximal motif of class 1 cytokine receptors

<220>
 <221> misc_feature
 <222> (3)
 <223> Xaa equals any

<400> 82
 Trp Ser Xaa Trp Ser
 1 5

<210> 83
 <211> 86
 <212> DNA

<213> Artificial Sequence

<220>

<221> primer_bind

<223> forward primer useful for generation of a synthetic gamma
activation site (GAS) containing promoter element

<400> 83

gcgcctcgag atttccccga aatctagatt tccccgaaat gatttccccg aaatgatttc 60

cccgaatat ctgccatctc aattag 86

<210> 84

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<221> primer_bind

<223> reverse primer useful for generation of a synthetic gamma
activation site (GAS) containing promoter element

<400> 84

gcggcaagct ttttgcaaag cctaggc 27

<210> 85

<211> 271

<212> DNA

<213> Artificial Sequence

<220>

<221> misc_feature

<223> Synthetic GAS-SV40 promoter sequence

<400> 85

ctcgagattt ccccgaaatc tagatttccc cgaaatgatt tccccgaaat gatttccccg 60

aaatatctgc catctcaatt agtcagcaac catagtcccg cccctaactc cgcccatccc 120

gcccctaact cgcgccagtt cgcgccattc tccgcccacat ggctgactaa ttttttttat 180

ttatgcagag gccgaggccg cctcggcctc tgagctattc cagaagtagt gaggaggctt 240

ttttggaggc ctaggctttt gcaaaaagct t 271

<210> 86

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<221> primer_bind

<223> primer useful for generation of a EGR/SEAP reporter construct

<400> 86

gcgctcgagg gatgacagcg atagaacccc gg

32

<210> 87

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<221> primer_bind

<223> primer useful for generation of a EGR/SEAP reporter construct

<400> 87

gcgaagcttc gcgactcccc ggatccgcct c

31

<210> 88

<211> 12

<212> DNA

<213> Artificial Sequence

<220>

<221> misc_binding

<223> NF-KB binding site

<400> 88

ggggactttc cc

12

<210> 89

<211> 73

<212> DNA

<213> Artificial Sequence

<220>

<221> primer_bind

<223> forward primer useful for generation of a vector containing the
NF-KB promoter element

<400> 89

gcggcctcga ggggactttc ccggggactt tccggggact ttccgggact ttccatcctg 60

ccatctcaat tag 73

<210> 90

<211> 256

<212> DNA

<213> Artificial Sequence

<220>

<221> misc_feature

<223> Synthetic NF-KB/SV40 promoter

<400> 90

ctcgagggga ctttcccggg gactttccgg ggactttccg ggactttcca tctgccatct 60

caattagtca gcaaccatag tcccgccct aactccgcc atcccgcct taactccgcc 120

cagttccgcc cattctccgc cccatggctg actaattttt tttatttatg cagaggccga 180

UNITED STATES PATENT AND TRADEMARK OFFICE
CERTIFICATE OF CORRECTION

PATENT NO. : 6,994,857 B2
APPLICATION NO. : 09/833041
DATED : February 7, 2006
INVENTOR(S) : DCraig A. Rosen and William A. Haseltine

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It is certified that error appears in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

ggccgctcg gcctctgagc tattccagaa gtagtgagga ggcttttttg gaggcctagg 240
cttttgcaaa aagctt 256

In the Claims

Col. 313, line 22, in claim 1 (c), "amino and" should read -- amino --.

Col. 313, line 33, in claim 1 (e), "or fragment thereof and albumin" should read -- or fragment thereof, and albumin --.

Col. 313, line 55, in claim 1 (i), "proten" should read -- protein --.

Col. 316, line 17, in claim 22, "protein, or thereof" should read -- protein, or fragment thereof --.

Signed and Sealed this

Third Day of October, 2006



JON W. DUDAS
Director of the United States Patent and Trademark Office